

1646

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/08/816,011C

DATE: 02/14/2001  
TIME: 17:54:56

Input Set : A:\11420121.app  
Output Set: N:\CRF3\02142001\H816011C.raw

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ENTERED

3 <110> APPLICANT: Pausch, Mark H  
4 Price, Laura A  
6 <120> TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
7 AND METHODS OF USING SAME  
9 <130> FILE REFERENCE: 01142.0122 SEQUENCE LISTING  
11 <140> CURRENT APPLICATION NUMBER: 08/816,011C  
12 <141> CURRENT FILING DATE: 1997-03-11  
14 <150> PRIOR APPLICATION NUMBER: 08/332,312  
15 <151> PRIOR FILING DATE: 1994-10-31  
17 <150> PRIOR APPLICATION NUMBER: PCT/US95/14364  
18 <151> PRIOR FILING DATE: 1995-10-25  
20 <160> NUMBER OF SEQ ID NOS: 64  
22 <170> SOFTWARE: PatentIn Ver. 2.1  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 2441  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Drosophila melanogaster  
29 <400> SEQUENCE: 1  
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31 ctttaaaaga aaaaaaaaaatataagtaaa aactacaaac cacacagcga aaggcgaaaag 120  
32 caacgggttcc tgcgagtgttatttttttttttcaacaatttttgatcgta gtgcgacaat 180  
33 cgcgcgagca tgcgcgcgaa tgcgatggatc ctgctgctca tcttctacat atcctacctg 240  
34 atgttcgggg cggcaatcta ttacatatt gagcacggcg aggagaagat atcgcgcgcc 300  
35 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct ggcgcgacaag 360  
36 aatacgacca cacaggatga gattcttcaa cggatctcgg attactgtga caaacgggtt 420  
37 acattgccgc cgacatatga tgatacgccc tacacgtgga ccttctaoca tgccttcttc 480  
38 ttgcgcttca cggtttgctc cacggtgga tatgggaata tatcgccaac caccttcgcc 540  
39 ggacggatga tcatgatcgc gtattcgggt attggcatcc cgtcaatgg tatcctcttt 600  
40 gccggcctcg gcgaatactt tggacgtacg tttgaagcga tctacagag ctacaaaaag 660  
41 tacaagatgt ccacggatat gcactatgct ccgccgcagc tgggattgat caccacgggtg 720  
42 gtgattgccc tgattccggg aatagctctc ttcttggtgc tgcctgcgt ggggtgttcac 780  
43 ctacttcgag aactgggcct atcttccatc tgcgtgtact acagctatgt gaccaccaca 840  
44 acaattggat tgggtgacta tgtgcccaca tttggagcca accagcccaa ggaagtccgc 900  
45 ggcgtggtcg tgggtctatca gatctttgtg atcgtgtggt tcatcttctc gctgggatat 960  
46 cttgtgatga tcatgacatt tatcactcgg gccctccaga gcaagaagct ggcataacctg 1020  
47 gagcagcagt tgcctccaa cctgaaggcc acacagaatc gcatctggtc tggcgtcacc 1080  
48 aaggatgtgg gctacctccg gcgaatgctc aacgagctgt acatcctcaa agtgaagcct 1140  
49 gtgtacaccg atgtagatat cgcctacaca ctgccacgtt ccaattcgtg tccggatctg 1200  
50 agcatgtacc gcgtggagcc ggcctccatt cccagccgga agagggcatt ctccgtgtgc 1260  
51 gccgacatgg ttggcgccca aaggaggcgg ggcatggtac acgccaattc cgatacggat 1320  
52 ctaaccaaac tggatcgcca gaagacattc gagacggcgg aggcgtacca ccagaccacc 1380  
53 gatttgctgg ccaagggtgt caacgcactg gccacggtga agccaccgcc ggcggaacag 1440  
54 gaagatgcgg ctctctatgg tggctatcat ggcttctccg actccagat cctggccagc 1500  
55 gaatggtcgt tctcgacggc caacgagttc acatcaccgc gacgtccaag agcacgtgcc 1560  
56 tgctccgatt tcaatctgga ggcacctcgc tggcagagcg agaggccact gcgttcgagc 1620  
57 cacaacgaat ggacatggag cggcgacaac cagcagatcc agaggcatt caaccagcgc 1680  
58 tacaaggagc agcagcgtgc caacggagca gccaaactcga ccatggtcca tctggagccg 1740

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59 gatgcttttg aggagcagct gagaacaat caccgggtgc cggtcgcgtc aagaagttct 1800
60 ccatgccgga tggctctgca cgtctgtttc ccttcagaa gaagcaccoc tgcagagatc 1860
61 tggagcgcaa gttgtccgtg gtctcgggtac ccgagggtgt catctcgag gaagccagat 1920
62 ccccgctgga ctactacatc aacacgggtca cggcggcctc cagtcaatcc tatttgcgca 1980
63 acggacgcgg tccgccaccg cccttcgaat cgaatggcag cttggccagc ggcggcggcg 2040
64 ggctaacgaa catgggcttc cagatggagg atggagcaac cccgccatcg gcattggggcg 2100
65 gtggagccta tcaacgcaag gcggtctgtg gcaagcgccg acgcgagagc atctacaccc 2160
66 agaataaagc cccatccgct cgcgggggca gcatgtatcc gccgaccgag cagccttgg 2220
67 cccagatgca gatgcgacgc ggcagcttgg caaccagtgg ctctggatcg gcggccatgg 2280
68 cggcagtggc cgcgcgtcgt ggcagcctct tcccagctac agcatcggca tcctcgtga 2340
69 cctctgctcc gcgccgaagc agcatattct cggttacctc cgaagaggat atgaatgtgc 2400
70 tggagcagac gaccattgag gatctgattc gtgcgctcga g 2441

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73 <210> SEQ ID NO: 2

74 <211> LENGTH: 618

75 <212> TYPE: PRT

76 <213> ORGANISM: Drosophila melanogaster

78 <400> SEQUENCE: 2

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79 Met Ser Pro Asn Arg Trp Ile Leu Leu Ile Phe Tyr Ile Ser Tyr
80 1 5 10 15
82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
83 20 25 30
85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
86 35 40 45
88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
89 50 55 60
91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
92 65 70 75 80
94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
95 85 90 95
97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
98 100 105 110
100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
101 115 120 125
103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
104 130 135 140
106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
107 145 150 155 160
109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
110 165 170 175
112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
113 180 185 190
115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
116 195 200 205
118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
119 210 215 220
121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
122 225 230 235 240
124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
125 245 250 255

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127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
128          260          265          270
130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
131          275          280          285
133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
134          290          295          300
136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
137 305          310          315          320
139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
140          325          330          335
142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
143          340          345          350
145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
146          355          360          365
148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
149          370          375          380
151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
152 385          390          395          400
154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
155          405          410          415
157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
158          420          425          430
160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
161          435          440          445
163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
164          450          455          460
166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
167 465          470          475          480
169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
170          485          490          495
172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
173          500          505          510
175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
176          515          520          525
178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
179          530          535          540
181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
182 545          550          555          560
184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
185          565          570          575
187 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
188          580          585          590
190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
191          595          600          605
193 Met Ala Ala Trp Pro Ala Ala Ala Gly
194          610          615
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1011
199 <212> TYPE: DNA

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200 <213> ORGANISM: Caenorhabditis elegans
202 <400> SEQUENCE: 3
203 atgtccgatac agctgtttgt cgcatttgag aagtatttct tgacgagtaa cgaggtaag 60
204 aagaatgcag caacggagac atggacattt tcatcgcca tttctttgc cgtaaccgtc 120
205 gtactacca tcggatacgg taatccagtt ccagtgacaa acattggacg gatattggtg 180
206 atattgttct ccttgcttgg aatacctcta acactgggta ccacgctga cttggcaggt 240
207 aaattccctat ctgaacatct tgtttggtg tatggaaact atttgaaatt aaaaatctc 300
208 atattgtcac gacatcgaaa agaacggaga gagcacgttt gtgagcactg tcacagtcac 360
209 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
210 attctgatag tatatacagc gtttggcggg gtcctaagt caaaattaga gccgtggtct 480
211 ttcttcaactt cattctactg gtccttcatt acaatgacta ctgtcgggtt tggcgacttg 540
212 atgcccgaaa gggacggata catgtatata atattgctct atatcatttt aggtaaattt 600
213 tcaatgaaaa aaaaacaaaa attcaaaaata tttttaggtc ttgcaataac tacaatgtgc 660
214 attgatttgg taggagtaca gtatattcga aagattcatt atttcggaag aaaaattcaa 720
215 gacgctagat ctgcattggc gttttagga ggaaggtag tccttgatc agaactctac 780
216 gcaaatttaa tgcaaaagcg agctcgtaac atgtcccgag aagcttttat agtggagaat 840
217 ctctatgttt ccaaacacat cataccattc ataccaactg atatccgatg tattcgatat 900
218 attgatcaaa ctgccgatgc tgctaccatt tccacgcat cgtctgcaat tgatatgcaa 960
219 agttgtagat ttgtgcattc aagatatctt ctcaatcgtg cattcaataa g 1011
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 336
224 <212> TYPE: PRT
225 <213> ORGANISM: Drosophila melanogaster
227 <400> SEQUENCE: 4
228 Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
229 1 5 10 15
231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
232 20 25 30
234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
235 35 40 45
237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
238 50 55 60
240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
241 65 70 75 80
243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
244 85 90 95
246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
247 100 105 110
249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
250 115 120 125
252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
253 130 135 140
255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
256 145 150 155 160
258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
259 165 170 175
261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
262 180 185 190
264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe

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```

265          195          200          205
267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
268          210          215          220
270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
271 225          230          235          240
273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
274          245          250          255
276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
277          260          265          270
279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
280          275          280          285
282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
283          290          295          300
285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
286 305          310          315          320
288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
289          325          330          335
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 51
297 <212> TYPE: DNA
298 <213> ORGANISM: Caenorhabditis elegans
300 <400> SEQUENCE: 5
301 tccattttct ttgccgtaac cgtcgtcact accatcggat acggtaatcc a          51
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 51
306 <212> TYPE: DNA
307 <213> ORGANISM: Caenorhabditis elegans
309 <400> SEQUENCE: 6
310 tcattctact ggctcttcat tacaatgact actgtcgggt ttggcgactt g          51
313 <210> SEQ ID NO: 7
314 <211> LENGTH: 24
315 <212> TYPE: PRT
316 <213> ORGANISM: Drosophila melanogaster
318 <400> SEQUENCE: 7
319 Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
320 1          5          10          15
322 Arg Cys Val Thr Asp Glu Cys Pro
323          20
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 24
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 8
332 Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
333 1          5          10          15
335 Arg Cys Val Thr Glu Gln Cys Ala
336          20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 24

```

FYI

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY                      DATE: 02/14/2001  
PATENT APPLICATION:    US/08/816,011C              TIME: 17:54:57

Input Set : A:\11420121.app  
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L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51  
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53  
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53  
L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53  
L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54  
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56  
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56  
L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57  
L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58  
L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60  
L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61  
L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64